



SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
TISSUE

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<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 296

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
 130 135 140
 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
 145 150 155 160
 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 165 170 175
 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 180 185 190
 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 195 200 205
 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 210 215 220
 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
 225 230 235 240
 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
 245 250 255
 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
 260 265 270
 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
 275 280 285
 Gln Lys Tyr Cys Cys Ser Arg Lys
 290 295

<210> 2

<211> 1070

<212> DNA

<213> Homo sapiens

<400> 2

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 tccgtgcgga tgagggactt gcggaatcca cacccttctt cagcgttcct gaacctgatt 180
 ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
 gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgagag ctccagccat 300
 gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttggtga ataccccatg 360
 acactgtcat tggcggccgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc 420

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ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg 480
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cggtttggtt tccctgcatt cagcggcatc tctcgactga cctggctggt ctccctcttt 600
ggggagcttt ctcttggtgc tgccactttg gaagagcgaa aggaagatca gtatatgaaa 660
atgacagtgt gtctggagac agagaagaaa agtccactgt catggattga agaaaaagga 720
cctgggtctaa aacgaaacag atattttaagc ttccatttca agtctgggtc cttggagaat 780
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aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
tgcttggggc ttgcagaaga aatccagaaa tattgctgtt caaggaagta agaggaggag 960
gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
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<210> 3

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3

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Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
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Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
          20              25              30

```

```

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
          35              40              45

```

```

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
          50              55              60

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```

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
          65              70              75              80

```

```

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
          85              90              95

```

```

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
          100              105              110

```

```

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
          115              120              125

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```

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
          130              135              140

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```

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
          145              150              155              160

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Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys
290 295

<210> 4

<211> 295

<212> PRT

<213> Rattus norvegicus

<400> 4

Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
1 5 10 15

Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
20 25 30

Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
35 40 45

Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
50 55 60

Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu

65		70		75		80									
Asp	Tyr	Ile	Arg	Gln	Phe	Leu	Gln	Ala	Gly	Lys	His	Val	Leu	Val	Glu
			85						90					95	
Tyr	Pro	Met	Thr	Leu	Ser	Phe	Ala	Ala	Ala	Gln	Glu	Leu	Trp	Glu	Leu
			100					105					110		
Ala	Ala	Gln	Lys	Gly	Arg	Val	Leu	His	Glu	Glu	His	Val	Glu	Leu	Leu
		115					120					125			
Met	Glu	Glu	Phe	Glu	Phe	Leu	Arg	Arg	Glu	Val	Leu	Gly	Lys	Glu	Leu
	130						135				140				
Leu	Lys	Gly	Ser	Leu	Arg	Phe	Thr	Ala	Ser	Pro	Leu	Glu	Glu	Glu	Arg
145					150					155					160
Phe	Gly	Phe	Pro	Ala	Phe	Ser	Gly	Ile	Ser	Arg	Leu	Thr	Trp	Leu	Val
			165					170						175	
Ser	Leu	Phe	Gly	Glu	Leu	Ser	Leu	Ile	Ser	Ala	Thr	Leu	Glu	Glu	Arg
		180						185					190		
Lys	Glu	Asp	Gln	Tyr	Met	Lys	Met	Thr	Val	Gln	Leu	Glu	Thr	Gln	Asn
	195						200					205			
Lys	Gly	Leu	Leu	Ser	Trp	Ile	Glu	Glu	Lys	Gly	Pro	Gly	Leu	Lys	Arg
	210					215					220				
Asn	Arg	Tyr	Val	Asn	Phe	Gln	Phe	Thr	Ser	Gly	Ser	Leu	Glu	Glu	Val
225					230					235					240
Pro	Ser	Val	Gly	Val	Asn	Lys	Asn	Ile	Phe	Leu	Lys	Asp	Gln	Asp	Ile
			245					250					255		
Phe	Val	Gln	Lys	Leu	Leu	Asp	Gln	Val	Ser	Ala	Glu	Asp	Leu	Ala	Ala
		260						265					270		
Glu	Lys	Lys	Arg	Ile	Met	His	Cys	Leu	Gly	Leu	Ala	Ser	Asp	Ile	Gln
	275						280					285			
Lys	Leu	Cys	His	Gln	Lys	Lys									
	290					295									

<210> 5

<211> 1081

<212> DNA

<213> Rattus norvegicus

<400> 5

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gaaatttgga gtggtagtgg ttggtggtgg cagagctggc tcggtgaggc tgagggactt 180
gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaagagat 300
tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca 420
ggagctgtgg gagctggccg cacagaaagg gagagtcctg catgaggagc acgtggaact 480
cttgatggag gaattcgaat tcctgagaag agaagtgttg gggaaagagc tactgaaagg 540
gtctcttcgc ttcacagcta gccactgga agaagagaga tttggcttcc ctgcgttcag 600
cggcatttct cgcctgacct ggctgggtctc cctcttcggg gagctttctc ttatttctgc 660
caccttgaa gagcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagaccca 720
gaacaagggg ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
tgtaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtaataa 840
gaacattttc ctgaaagatc aggatatatt tgttcagaag ctcttagacc aggtctctgc 900
agaggacctg gctgctgaga agaagcgcat catgcattgc ctggggctgg ccagcgacat 960
ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
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a 1081
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<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: hydrophobic
domain of BVR

<220>

<221> PEPTIDE

<222> (2)

<223> where X is any aa

<400> 6

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Phe Xaa Val Val Val Val
  1                      5
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<210> 7

<211> 6

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleotide
binding domain of BVR

<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (4)..(5)
<223> where X is any aa

<400> 7
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oxidoreductase domain of BVR

<400> 8
Ala Gly Lys His Val Leu Val Glu
1 5

<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: leucine
zipper of BVR

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> where X is any aa

<220>

<221> PEPTIDE
<222> (9)..(14)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (16)..(21)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (23)..(28)
<223> where X is any aa

<400> 9
Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
20 25

<210> 10
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 10
Ser Arg Arg
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<210> 11
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: kinase motif
of BVR

<400> 11
Lys Gly Ser
1

<210> 12
 <211> 3
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: kinase motif
 of BVR

 <220>
 <221> PEPTIDE
 <222> (3)
 <223> where X is any aa

 <400> 12
 Phe Gly Xaa
 1

 <210> 13
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: nuclear
 localization signal of BVR

 <400> 13
 Gly Leu Lys Arg Asn Arg Tyr
 1 5

 <210> 14
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: methylation
 site of BVR

 <400> 14
 Pro Gly Leu Lys Arg
 1 5

<210> 15
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: zinc finger
 domain of BVR

 <220>
 <221> PEPTIDE
 <222> (3)..(12)
 <223> where X is any aa

 <400> 15
 His Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys
 1 5 10

 <210> 16
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: protein
 kinase C enhancing domain

 <220>
 <221> PEPTIDE
 <222> (5)
 <223> where X is any aa

 <400> 16
 Lys Lys Arg Ile Xaa His Cys
 1 5

 <210> 17
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: protein
 kinase C inhibiting domain

<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa

<220>
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<222> (5)..(7)
<223> where X is any aa

<400> 17
Gln Lys Xaa Cys Xaa Xaa Xaa Lys
1 5